

J. Hines

1641

PAGE: 1

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/961,083**

DATE: 01/29/1999
TIME: 17:50:39

INPUT SET: S30408.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/961,083DATE: 01/29/1999
TIME: 17:50:40

INPUT SET: S30408.raw

47 (vi) CURRENT APPLICATION DATA:
48 (A) APPLICATION NUMBER:
50 (B) FILING DATE:
52 (C) CLASSIFICATION:
54
55
56
57 (vii) PRIOR APPLICATION DATA:
58 (A) APPLICATION NUMBER:
60 (B) FILING DATE:
62
63
64
65 (viii) ATTORNEY/AGENT INFORMATION:
66 (A) NAME: Brookes, A. Anders
68 (B) REGISTRATION NUMBER: 36,373
70 (C) REFERENCE/DOCKET NUMBER: PB340P2
72
73
74
75 (vi) TELECOMMUNICATION INFORMATION:
76 (A) TELEPHONE: (301) 309-8504
78 (B) TELEFAX: (301) 309-8512
80
81
82
83
84
85
86
87 (2) INFORMATION FOR SEQ ID NO: 1:
88 (i) SEQUENCE CHARACTERISTICS:
89 (A) LENGTH: 1999 base pairs
90 (B) TYPE: nucleic acid
91 (C) STRANDEDNESS: double
92 (D) TOPOLOGY: linear
93
94
95
96
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
98
99 TAAAAATCTAC GACAATAAAA ATCAACTCAT TGCTGACTTG GGTTCTGAAC GCCGCGTCAA

INPUT SET: S30408.raw

100 TGCCCAAGCT AATGATATTG CCACAGATTT GGTAAAGGCA ATCGTTTCTA TCGAAGACCA 120
101 TCGCTTCTTC GACCACAGGG GGATTGATAC CATCCGTATC CTGGGAGCTT TCTTGCGCAA 180
102
103
104 TCTGCAAAGC AATTCCCTCC AAGGTGGATC AACTCTCACC CAACAGTTGA TTAAGTTGAC 240
105 TTACTTTCA ACTTCGACTT CCGACCAGAC TATTCTCGT AAGGCTCAGG AAGCTTGGTT 300
106
107 AGCGATTCAG TTAGAACAAA AAGCAACCAA GCAAGAAATC TTGACCTACT ATATAAATAA 360
108 GGTCTACATG TCTAATGGGA ACTATGGAAT GCAGACAGCA GCTCAAAACT ACTATGGTAA 420
109
110 AGACCTCAAT AATTAAAGTT TACCTCAGTT AGCCTTGCTG GCTGGAATGC CTCAGGCACC 480
111
112 AAACCAATAT GACCCCTATT CACATCCAGA AGCAGCCCAA GACCGCCGAA ACTTGGTCTT 540
113 ATCTGAAATG AAAATCAAG GCTACATCTC TGCTGAACAG TATGAGAAAG CAGTCAATAC 600
114
115 ACCAATTACT GATGGACTAC AAAGTCTCAA ATCAGCAAGT AATTACCCTG CTTACATGGA 660
116 TAATTACCTC AAGGAAGTCA TCAATCAAGT TGAAGAAGAA ACAGGCTATA ACCTACTCAC 720
117 AACTGGGATG GATGTCTACA CAAATGTAGA CCAAGAAGCT CAAAAACATC TGTGGGATAT 780
118 TTACAATACA GACGAATACG TTGCCTATCC AGACGATGAA TTGCAAGTCG CTTCTACCAT 840
119
120 TGTTGATGTT TCTAACGGTA AAGTCATTGC CCAGCTAGGA GCACGCCATC AGTCAAGTAA 900
121
122 TGTTCCTTC GGAATTAACC AAGCAGTAGA AACAAACCGC GACTGGGAT CAACTATGAA 960
123 ACCGATCACA GACTATGCTC CTGCCTTGGA GTACGGTGTAC TACGATTCAA CTGCTACTAT 1020
124 CGTTCACGAT GAGCCCTATA ACTACCCTGG GACAAATACT CCTGTTTATA ACTGGGATAG 1080
125
126 GGGCTACTTT GGCAACATCA CCTTGCAATA CGCCCTGCAA CAATCGCGAA ACGTCCCAGC 1140
127 CGTGGAAACT CTAAACAAGG TCGGACTCAA CCGCGCCAAG ACTTTCCTAA ATGGTCTAGG 1200
128
129 AATCGACTAC CCAAGTATTG ACTACTCAA TGCCATTCA AGTAACACAA CCGAATCAGA 1260
130
131 CAAAAAATAT GGAGCAAGTA GTGAAAAGAT GGCTGCTGCT TACGCTGCCT TTGCAAATGG 1320
132
133 TGGAACTTAC TATAAACCAA TGTATATCCA TAAAGTCGTC TTTAGTGATG GGAGTGAAAA 1380
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135 AGAGTTCTCT AATGTCGGAA CTCGTGCCAT GAAGGAAACG ACAGCCTATA TGATGACCGA 1440
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137 CATGATGAAA ACAGTCTTGA CTTATGGAAC TGGACGAAAT GCCTATCTTG CTTGGCTCCC 1500
138
139 TCAGGCTGGT AAAACAGGAA CCTCTAACTA TACAGACGAG GAAATTGAAA ACCACATCAA 1560
140 GACCTCTCAA TTTGTAGCAC CTGATGAACT ATTTGCTGGC TATACGCGTA AATATTCAAT 1620
151
152

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/961,083DATE: 01/29/1999
TIME: 17:50:40

INPUT SET: S30408.raw

153 GGCTGTATGG ACAGGCTATT CTAACCGTCT GACACCCTT GTAGGCAATG GCCTTACGGT 1680
 154 CGCTGCCAAA GTTTACCGCT CTATGATGAC CTACCTGTCT GAAGGAAGCA ATCCAGAAGA 1740
 155 TTGGAATATA CCAGAGGGC TCTACAGAAA TGGAGAATTG GTATTAAAAA ATGGTGCTCG 1800
 156 TTCTACGTGG AACTCACCTG CTCCACAAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860
 157 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACTCCA AGCACAAATA ATAGTACGAC 1920
 158 TACCAATCCT AACAAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980
 159 TCCTCAACCA GCACAACCA 1999
 160
 161
 162
 163
 164
 165
 166
 167 (2) INFORMATION FOR SEQ ID NO:2:
 168
 169 (i) SEQUENCE CHARACTERISTICS:
 170 (A) LENGTH: 666 amino acids
 171 (B) TYPE: amino acid
 172 (C) STRANDEDNESS: single
 173 (D) TOPOLOGY: linear
 174
 175 (ii) MOLECULE TYPE: protein
 176
 177
 178
 179
 180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 181
 182 Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
 183 1 5 10 15
 184
 185 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
 186 20 25 30
 187
 188 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
 189 35 40 45
 190
 191 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
 192 50 55 60
 193
 194 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
 195 65 70 75 80
 196
 197 Tyr Phe Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
 198 85 90 95
 199
 200 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
 201 100 105 110
 202
 203 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
 204 115 120 125
 205

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/961,083

DATE: 01/29/1999
 TIME: 17:50:41

INPUT SET: S30408.raw

206 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn
 207 130 135 140
 208
 209 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro
 210 145 150 155 160
 211
 212 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg
 213 165 170 175
 214
 215 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu
 216 180 185 190
 217
 218 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser
 219 195 200 205
 220
 221 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys
 222 210 215 220
 223
 224 Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr
 225 230 235 240
 226
 227 Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His
 228 245 250 255
 229
 230 Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp
 231 260 265 270
 232
 233 Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val
 234 275 280 285
 235
 236 Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly
 237 290 295 300
 238
 239 Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys
 240 305 310 315 320
 241
 242 Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser
 243 325 330 335
 244
 245 Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn
 246 340 345 350
 247
 248 Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu
 249 355 360 365
 250
 251 Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu
 252 370 375 380
 253
 254 Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly
 255 385 390 395 400
 256
 257 Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr
 258 405 410 415

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/961,083**

DATE: 01/29/1999
TIME: 17:50:41

INPUT SET: S30408.raw

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Original Text